



## **RAW SEQUENCE LISTING** **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/500,601  
Source: PG/10  
Date Processed by STIC: 7/8/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.2 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/efb/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):  
U.S. Patent and Trademark Office, 220 20<sup>th</sup> Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby Room 1B03, Arlington, VA 22202

Revised 05/17/04

## Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	SERIAL NUMBER: <u>10/500,601</u>
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 <u>    </u> Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 <u>    </u> Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 <u>    </u> Misaligned Amino Numbering	The numbering under each 5 <sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 <u>    </u> Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 <u>    </u> Variable Length	Sequence(s) <u>1</u> contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 <u>    </u> PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) <u>            </u> . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 <u>    </u> Skipped Sequences (OLD RULES)	Sequence(s) <u>      </u> missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped  Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 <u>    </u> Skipped Sequences (NEW RULES)	Sequence(s) <u>      </u> missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 <u>    </u> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 <u>   </u> Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 <u>   </u> Use of <220>	Sequence(s) <u>      </u> missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 <u>   </u> PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 <u>   </u> Misuse of n/Xaa	"n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid	



PCT

## RAW SEQUENCE LISTING

DATE: 07/08/2004

PATENT APPLICATION: US/10/500,601

TIME: 16:29:28

Input Set : A:\29808PW1-GE.APP.txt

Output Set: N:\CRF4\07082004\J500601.raw

2 <110> APPLICANT: Repp Prof., Reinald  
 4 <120> TITLE OF INVENTION: Methods for detecting nucleic acids using solid phase  
 5 bound primers and cleaving the products of a cyclic  
 6 amplification reaction (Trap Release Primer  
 7 Amplification (TRamp))  
 9 <130> FILE REFERENCE: 29808PWO\_RI  
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/500,601  
 C--> 12 <141> CURRENT FILING DATE: 2004-06-30  
 14 <150> PRIOR APPLICATION NUMBER: DE10164219.9  
 15 <151> PRIOR FILING DATE: 2001-12-31  
 17 <160> NUMBER OF SEQ ID NOS: 1  
 19 <170> SOFTWARE: PatentIn Ver. 2.1  
 21 <210> SEQ ID NO: 1  
 22 <211> LENGTH: 32  
 23 <212> TYPE: DNA  
 24 <213> ORGANISM: Artificial Sequence  
 26 <220> FEATURE:  
 27 <221> NAME/KEY: misc\_binding  
 28 <222> LOCATION: (1)  
 29 <223> OTHER INFORMATION: Any Sequence  
 31 <220> FEATURE:  
 32 <221> NAME/KEY: misc\_binding  
 33 <222> LOCATION: (32)  
 34 <223> OTHER INFORMATION: Any Sequence  
 36 <220> FEATURE:  
 37 <223> OTHER INFORMATION: Description of the artificial sequence: PCR-primer  
 39 <400> SEQUENCE: 1  
 W--> 40 ntttgtctcg agtgttttca ctcgagactt tn

Does Not Comply  
Corrected Dikette Needed

? "n" can only represent a single nucleotide

(variable length is not permitted)

See item 5

on Error  
summary  
sheet

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RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/10/500,601

DATE: 07/08/2004  
TIME: 16:29:29

Input Set : A:\29808PW1-GE.APP.txt  
Output Set: N:\CRF4\07082004\J500601.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 1,32

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/500,601

DATE: 07/08/2004

TIME: 16:29:29

Input Set : A:\29808PW1-GE.APP.txt

Output Set: N:\CRF4\07082004\J500601.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:40 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0